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(54) **COMBINATION VACCINE**

(75) Inventors: **Jorge Garcia Lara**, Sheffield (GB);  
**Simon Foster**, Hathersage (GB)

(73) Assignee: **Absynth Biologics Limited**, Sheffield  
(GB)

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None

See application file for complete search history.

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Primary Examiner — Jennifer Graser

(74) Attorney, Agent, or Firm — Seed IP Law Group PLLC

(57) **ABSTRACT**

The disclosure relates to a composition comprising two or  
more immunogenic staphylococcal polypeptides and a mul-  
tivalent vaccine composition comprising the immunogenic  
staphylococcal polypeptides.

**12 Claims, No Drawings**

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## COMBINATION VACCINE

## REFERENCE TO RELATED APPLICATIONS

This application is the US national phase entry of International Patent Application No. PCT/GB2012/050791, filed Apr. 11, 2012, which claims priority to GB Patent Application No. 1106162.9, filed Apr. 12, 2011.

## FIELD OF THE INVENTION

The disclosure relates to a composition comprising two or more immunogenic staphylococcal polypeptides and a multivalent vaccine composition comprising the immunogenic staphylococcal polypeptides in the prevention or treatment of staphylococcal infections in humans and animals.

## BACKGROUND

Vaccines protect against a wide variety of infectious diseases. Many modern vaccines are therefore made from protective antigens of the pathogen, which are isolated by molecular cloning and purified. These vaccines are known as 'subunit vaccines'. The development of subunit vaccines has been the focus of considerable research in recent years. The emergence of new pathogens and the growth of antibiotic resistance have created a need to develop new vaccines and to identify further candidate molecules useful in the development of subunit vaccines. Likewise the discovery of novel vaccine antigens from genomic and proteomic studies is enabling the development of new subunit vaccine candidates, particularly against bacterial pathogens. However, although subunit vaccines tend to avoid the side effects of killed or attenuated pathogen vaccines, their 'pure' status means that subunit vaccines do not always have adequate immunogenicity to confer protection.

An approach to improve the efficacy of vaccine compositions is to provide multivalent vaccines comprising dominant antigens that provoke both a B cell and T cell response thereby mounting a more rigorous immune response in the subject receiving the vaccine. A typical multivalent vaccine might be a whole cell vaccine comprising multiple antigenic molecules. For example the *Bacillus Calmette Guerin* ["BCG"] vaccine includes an attenuated *Mycobacterium bovis* strain that provokes protective immunity in humans. For many pathogens chemical or heat inactivation while it may give rise to vaccine immunogens that confer protective immunity also gives rise to side effects such as fever and injection site reactions. In the case of bacteria, inactivated organisms tend to be so toxic that side effects have limited the application of such crude vaccine immunogens and therefore vaccine development has lagged behind drug-development. Moreover, effective vaccine development using whole cell inactivated organisms suffers from problems of epitope masking, immunodominance, low antigen concentration and antigen redundancy.

Currently there is no effective vaccination procedure to prevent or treat *Staphylococcus aureus* infection. *S. aureus* is a bacterium whose normal habitat is the epithelial lining of the nose in about 20-40% of normal healthy people and is also commonly found on people's skin usually without causing harm. However, in certain circumstances, particularly when skin is damaged, this pathogen can cause infection. This is a particular problem in hospitals where patients may have surgical procedures and/or be taking immunosuppressive drugs. These patients are much more vulnerable to infection with *S. aureus* because of the treatment they have received. Antibiotic

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resistant strains of *S. aureus* have arisen since their wide spread use in controlling microbial infection. Methicillin resistant strains are prevalent and many of these resistant strains are also resistant to several other antibiotics.

*S. aureus* is therefore a major human pathogen capable of causing a wide range of diseases some of which are life threatening diseases including septicaemia, endocarditis, arthritis and toxic shock. This ability is determined by the versatility of the organism and its arsenal of components involved in virulence. At the onset of infection, and as it progresses, the needs and environment of the organism changes and this is mirrored by a corresponding alteration in the virulence determinants which *S. aureus* produces. At the beginning of infection it is important for the pathogen to adhere to host tissues and so a large repertoire of cell surface associated attachment proteins are made. The pathogen also has the ability to evade host defenses by the production of factors that reduce phagocytosis or interfere with the ability of the cells to be recognised by circulating antibodies.

There is therefore a continuing need to identify staphylococcal antigens that are protective and can be used in multivalent vaccines. The combinations may be used in combination with non-protein immunogenic molecules such as polysaccharide antigens and anti-bacterial agents to provide a treatment regimen for control of staphylococcal infection. It is also within the scope of this disclosure to modify the treatment regimen to immunize subjects with a series of temporally separated administrations as an alternative to the administration of a single vaccine comprising multiple antigens.

## SUMMARY

This disclosure therefore relates to combination or multivalent immunogenic compositions and vaccines and their use in the prophylaxis and treatment of staphylococcal infections. We disclose polypeptides that individually are protective and are typically membrane spanning proteins that include an extracellular domain and are essential for staphylococcal cell growth. For example DivIB is an integral membrane protein comprising an intracellular domain, an intermembrane domain and an extracellular domain. DivIB and fragments thereof, provide protection from at least an *S. aureus* challenge in an animal model. The related gene DivIC is also an integral membrane protein the extracellular domain of which provokes protective immunity to staphylococcal infection. This disclosure also relates to antigens encoded by the genes PheP, YdiE and FtsL each of which have an extramembranous domain.

According to an aspect of the invention there is provided an immunogenic composition comprising two or more different polypeptides wherein said polypeptides are encoded by different staphylococcal genes selected from the group consisting of:

- i) a polypeptide, or immunogenic fragment thereof, comprising or consisting of the amino acid sequence as represented in SEQ ID NO: 20;
- ii) a polypeptide, or immunogenic fragment thereof, comprising or consisting of the amino acid sequence as represented in SEQ ID NO: 21;
- iii) a polypeptide, or immunogenic fragment thereof, comprising or consisting of the amino acid sequence as represented in SEQ ID NO: 22;
- iv) a polypeptide, or immunogenic fragment thereof, comprising or consisting of the amino acid sequence as represented in SEQ ID NO: 23;

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v) a polypeptide, or immunogenic fragment thereof, comprising or consisting of the amino acid sequence as represented in SEQ ID NO: 24; or

vi) a modified staphylococcal polypeptide wherein said polypeptide is a staphylococcal polypeptide variant of the amino acid sequences presented in SEQ ID NO: 20, 21, 22, 23 or 24, wherein said sequences are modified by addition, deletion or substitution of one or more amino acid residues which modified polypeptides have retained or enhanced immunogenicity when compared to the polypeptide as represented in SEQ ID NO: 20, 21, 22, 23 or 24.

A modified staphylococcal polypeptide or variant staphylococcal polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions, truncations that may be present in any combination. Among preferred variants are those that vary from a reference polypeptide by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid by another amino acid of like characteristics. The following non-limiting list of amino acids are considered conservative replacements (similar): a) alanine, serine, and threonine; b) glutamic acid and aspartic acid; c) asparagine and glutamine d) arginine and lysine; e) isoleucine, leucine, methionine and valine and f) phenylalanine, tyrosine and tryptophan. Most highly preferred are variants that retain or enhance the immunogenicity and/or activity as the reference polypeptide from which it varies.

In one embodiment, the variant polypeptides have at least 80-89% sequence identity, more preferably at least 90% identity, even more preferably at least 95% identity, still more preferably at least 97% identity, and most preferably at least 99% identity with the full length amino acid sequences illustrated herein.

In a preferred embodiment of the invention said immunogenic composition comprises or consists essentially of 2, 3, 4 or 5 staphylococcal polypeptides.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 21, or antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 22, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 23, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided a composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 23 and 24, or an antigenic fragment thereof.

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In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 21 and 22, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 22 and 23, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 21 and 23, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 22 and 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 21 and 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 21, 23 and 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 22, 23 and 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 21, 22 and 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 21, 22 and 23, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 20, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 21, 22, 23 and 24, or an antigenic fragment thereof.

In an alternative preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 21, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 22, or an antigenic fragment thereof.

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In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 21, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 23, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 21, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 21, or an antigenic fragment thereof; and
- ii) a polypeptide comprising 23 and 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 21, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 22, and 23, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 21, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 22 and 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 21, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 22, 23 and 24, or an antigenic fragment thereof.

In an alternative preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 22, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 23 and 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 22, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 23, or an antigenic fragment thereof.

In a preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 22, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 24, or an antigenic fragment thereof.

In an alternative preferred embodiment of the invention there is provided an immunogenic composition comprising:

- i) a polypeptide comprising SEQ ID NO: 23, or an antigenic fragment thereof; and
- ii) a polypeptide comprising SEQ ID NO: 24, or an antigenic fragment thereof.

In a preferred embodiment of the invention said composition is a vaccine composition and includes at least one carrier and/or adjuvant.

#### DETAILED DESCRIPTION

Adjuvants (immune potentiators or immunomodulators) have been used for decades to improve the immune response

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to vaccine antigens. The incorporation of adjuvants into vaccine formulations is aimed at enhancing, accelerating and prolonging the specific immune response to vaccine antigens. Advantages of adjuvants include the enhancement of the immunogenicity of weaker antigens, the reduction of the antigen amount needed for a successful immunisation, the reduction of the frequency of booster immunisations needed and an improved immune response in elderly and immunocompromised vaccines. Selectively, adjuvants can also be employed to optimise a desired immune response, e.g. with respect to immunoglobulin classes and induction of cytotoxic or helper T lymphocyte responses. In addition, certain adjuvants can be used to promote antibody responses at mucosal surfaces. Aluminium hydroxide and aluminium or calcium phosphate has been used routinely in human vaccines.

Adjuvants can be classified according to their source, mechanism of action and physical or chemical properties. The most commonly described adjuvant classes are gel-type, microbial, oil-emulsion and emulsifier-based, particulate, synthetic and cytokines. More than one adjuvant may be present in the final vaccine product according to the invention. They may be combined together with a single antigen or all antigens present in the vaccine, or each adjuvant may be combined with one particular antigen. The origin and nature of the adjuvants currently being used or developed is highly diverse. For example, aluminium based adjuvants consist of simple inorganic compounds and PLG is a polymeric carbohydrate. MDP is derived from bacterial cell walls; saponins are of plant origin, squalene is derived from shark liver and recombinant endogenous immunomodulators are derived from recombinant bacterial, yeast or mammalian cells. There are several adjuvants licensed for veterinary vaccines, such as mineral oil emulsions that are too reactive for human use. Similarly, complete Freund's adjuvant, although being one of the most powerful adjuvants known, is not suitable for human use.

A carrier is an immunogenic molecule which, when bound to a second molecule augments immune responses to the latter. The term carrier is construed in the following manner. A carrier is an immunogenic molecule which, when bound to a second molecule augments immune responses to the latter. Some antigens are not intrinsically immunogenic yet may be capable of generating antibody responses when associated with a foreign protein molecule such as keyhole-limpet haemocyanin or tetanus toxoid. Such antigens contain B-cell epitopes but no T cell epitopes. The protein moiety of such a conjugate (the "carrier" protein) provides T-cell epitopes which stimulate helper T-cells that in turn stimulate antigen-specific B-cells to differentiate into plasma cells and produce antibody against the antigen.

The vaccine compositions of the invention can be administered by any conventional route, including injection, intranasal spray by inhalation of for example an aerosol or nasal drops. The administration may be, for example, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or intradermally. The vaccine compositions of the invention are administered in effective amounts. An "effective amount" is that amount of a vaccine composition that alone or together with further doses, produces the desired response. In the case of treating a particular bacterial disease the desired response is providing protection when challenged by an infective agent.

In a preferred embodiment of the invention said vaccine composition is adapted for administration as a nasal spray.

In a preferred embodiment of the invention said vaccine composition is provided in an inhaler and delivered as an aerosol.

The amounts of vaccine will depend, of course, on the individual patient parameters including age, physical condition, size and weight, the duration of the treatment, the nature of concurrent therapy (if any), the specific route of administration and like factors within the knowledge and expertise of the health practitioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used sufficient to provoke immunity; that is, the highest safe dose according to sound medical judgment. It will be understood by those of ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

The doses of vaccine administered to a subject can be chosen in accordance with different parameters, in particular in accordance with the mode of administration used and the state of the subject. In the event that a response in a subject is insufficient at the initial doses applied, higher doses (or effectively higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits.

In general, doses of vaccine are formulated and administered in effective immunizing doses according to any standard procedure in the art. Other protocols for the administration of the vaccine compositions will be known to one of ordinary skill in the art, in which the dose amount, schedule of injections, sites of injections, mode of administration and the like vary from the foregoing. Administration of the vaccine compositions to mammals other than humans, (e.g. for testing purposes or veterinary therapeutic purposes), is carried out under substantially the same conditions as described above. A subject, as used herein, is a mammal, preferably a human, and including a non-human primate, cow, horse, pig, sheep or goat.

The ratio of antigens may be varied in pair wise fashion. The ratio of each antigen may be 1:1, 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1 or 10:1 to optimize the response of the subject to particular combinations of antigen. For example the ratio of DivIB and YdiE may be varied as described above.

In a preferred embodiment of the invention there is provided a vaccine composition according to the invention that includes at least one additional anti-bacterial agent.

In a preferred embodiment of the invention said agent is a second different vaccine and/or immunogenic agent (for example a bacterial polypeptide and/or polysaccharide antigen).

According to a further aspect of the invention there is provided a composition comprising a nucleic acid molecule [s] comprising or consisting of nucleotide sequences of two or more different staphylococcal genes and encoding immunogenic polypeptides selected from the group consisting of:

- i) a nucleic acid molecule comprising or consisting of the nucleotide sequence as represented in SEQ ID NO: 1 or 6;
- ii) a nucleic acid molecule comprising or consisting of the nucleotide sequence as represented in SEQ ID NO: 2 or 7;
- iii) a nucleic acid molecule comprising or consisting of the nucleotide sequence as represented in SEQ ID NO: 3 or 8;
- iv) a nucleic acid molecule comprising or consisting of the nucleotide sequence as represented in SEQ ID NO: 4 or 9;

v) a nucleic acid molecule comprising or consisting of the nucleotide sequence as represented in SEQ ID NO: 5 or 10;

vi) a nucleic acid molecule comprising or consisting of a nucleotide sequence wherein said sequence is degenerate as a result of the genetic code to the nucleotide sequence defined in i-v above; or

vii) a nucleic acid molecule the complementary strand of which hybridizes under stringent hybridization conditions to the sequence in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 and wherein said nucleic acid molecule encodes a staphylococcal antigenic polypeptide.

Hybridization of a nucleic acid molecule occurs when two complementary nucleic acid molecules undergo an amount of hydrogen bonding to each other. The stringency of hybridization can vary according to the environmental conditions surrounding the nucleic acids, the nature of the hybridization method, and the composition and length of the nucleic acid molecules used. Calculations regarding hybridization conditions required for attaining particular degrees of stringency are discussed in Sambrook et al., *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 2001); and Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes Part I*, Chapter 2 (Elsevier, New York, 1993). The  $T_m$  is the temperature at which 50% of a given strand of a nucleic acid molecule is hybridized to its complementary strand. The following is an exemplary set of hybridization conditions and is not limiting:

Very High Stringency (Allows Sequences that Share at Least 90% Identity to Hybridize)

Hybridization: 5×SSC at 65° C. for 16 hours

Wash twice: 2×SSC at room temperature (RT) for 15 minutes each

Wash twice: 0.5×SSC at 65° C. for 20 minutes each

High Stringency (Allows Sequences that Share at Least 80% Identity to Hybridize)

Hybridization: 5×–6×SSC at 65° C.–70° C. for 16–20 hours

Wash twice: 2×SSC at RT for 5–20 minutes each

Wash twice: 1×SSC at 55° C.–70° C. for 30 minutes each

Low Stringency (Allows Sequences that Share at Least 50% Identity to Hybridize)

Hybridization: 6×SSC at RT to 55° C. for 16–20 hours

Wash at least twice: 2×–3×SSC at RT to 55° C. for 20–30 minutes each.

In a preferred embodiment of the invention said composition is a vaccine composition and includes and includes at least one carrier and/or adjuvant.

The nucleic acid or DNA combination vaccines comprise nucleic acid molecules that encode antigenic polypeptides as herein disclosed. The specific combinations of polypeptide antigens as represented by amino acid SEQ ID can be substituted for the corresponding nucleotide SEQ ID as herein disclosed in the manufacture of DNA vaccines.

According to a further aspect of the invention there is provided a combination vaccine according to the invention for use in the protection or treatment of a subject animal to a staphylococcal infection or condition that results from a staphylococcal infection.

In a preferred embodiment of the invention said staphylococcal infection is caused by a staphylococcal species selected from the group consisting of: *S. epidermidis*, *S. aureus*, *S. hominis*, *S. haemolyticus*, *S. warneri*, *S. capitis*, *S. saccharolyticus*, *S. auricularis*, *S. simulans*, *S. saprophyticus*, *S. cohnii*, *S. xylosus*, *S. hyicus*, *S. caprae*, *S. gallinarum*, *S. intermedius*,

In a further preferred embodiment of the invention said staphylococcal species is *S. aureus* or *S. epidermidis*.

In a preferred embodiment of the invention said subject is a human.

In an alternative preferred embodiment of the invention said subject is a non-human animal, preferably a livestock animal, for example cattle.

In a preferred embodiment of the invention said live stock animal is vaccinated against bacterial mastitis caused by staphylococcal bacterial cells.

In a preferred embodiment of the invention said life stock animal is a caprine animal (e.g. sheep, goat).

In a preferred embodiment of the invention said life stock animal is a bovine animal (e.g. a cow).

Staphylococcal mastitis is a serious condition that affects live stock and can result in considerable expense with respect to controlling the disease through administration of antibiotics and in terms of lost milk yield. The vaccine according to the invention provides cost effective control of bacterial, in particular staphylococcal mastitis.

Throughout the description and claims of this specification, the words "comprise" and "contain" and variations of the words, for example "comprising" and "comprises", means "including but not limited to", and is not intended to (and does not) exclude other moieties, additives, components, integers or steps.

Throughout the description and claims of this specification, the singular encompasses the plural unless the context otherwise requires. In particular, where the indefinite article is used, the specification is to be understood as contemplating plurality as well as singularity, unless the context requires otherwise.

Features, integers, characteristics, compounds, chemical moieties or groups described in conjunction with a particular aspect, embodiment or example of the invention are to be understood to be applicable to any other aspect, embodiment or example described herein unless incompatible therewith.

An embodiment of the invention will now be described by example only and with reference to the following FIGURES

Tables 3 and 4 illustrate the vaccination of a mouse model with a combination antigens of the extracellular domains of YdiE and DivIB compared to individual antigen vaccinations. Materials and Methods

Construction of Plasmids for the Overexpression in *E. coli* of the Extramembranous Fragments of the *S. aureus* Proteins

The PheP selected peptide was synthesized and conjugated through a cysteine at its C terminal to the carrier protein KLH to undertake as a chimeric protein used in vaccinations. The extramembranous fragments of YdiE, DivIB, DivIC and FtsL were PCR amplified from the chromosome of strain *S. aureus* SH1000 (Horsburgh M J, Aish J L, White I J, Shaw L, Lithgow J K, Foster S J: sigmaB modulates virulence determinant expression and stress resistance: characterization of a functional rsbU strain derived from *Staphylococcus aureus* 8325-4. *J Bacteriol* 2002, 184:5457-5467) using oligonucleotide pairs indicated on Table 1 according to the following PCR reaction conditions: 1 initial denaturation cycle of 94° C. for 4 min; 30 amplification cycles of denaturation 94° C. for 30 seconds, annealing 45° C. for 30 seconds, and extension at 72° C. for up to 2.5 minutes; finally, ongoing amplification rounds were allow to complete at 72° C. for 4 min.

The restrictions sites engineered within the oligonucleotides are also indicated in Table 1 (underlined; NcoI or XhoI). The amplified fragments were digested with the corresponding restriction enzymes (NcoI for the 5' end, and XhoI for the 3' end) and cloned into the equivalent sites of the pET-21d(+) expression vector from Novagen (Cat. No.

69743-3) and resulting in the overexpression plasmids indicated in Table 1 generating a T7-tagged (partial, at the N-terminal) and 6xHis-tagged (at the C-terminal end) form of the extramembranous fragments. In the SEQ IDs the T7- and His-tags are indicated in bold, and the extramembranous portion of the proteins of interest are underlined. The over expression plasmids were transferred into *E. coli* BL21 for over expression of the recombinant protein fragment.

The cloning of the PCR amplified fragment indicated above into the recipient pET21d(+) recipient plasmid vector at the NcoI and XhoI sites entailed the addition of hinge amino acids between the T7-tag and the extramembranous fragment, and between the latter and the His-tag. These amino acids are neither bold nor underlined in the SEQ IDs.

Over Expression of SEQ ID NO: 25-28

SEQ ID NOs 25 through 28 were over expressed from plasmids pGL597, pGL601, pALB26, and pALB27 in *E. coli* BL21 strain using Brain Heart Infusion Broth (CM0225, Oxoid, United Kingdom) in the presence of 100 µg/ml ampicillin and the Plac promoter gratuitous inducer IPTG (Isopropyl β-D-1-thiogalactopyranoside, 1 mM) for 4 to 6 hours at 37° C. and vigorous shaking. Following harvesting of the cells by centrifugation (5,000×g for 15 minutes at 4° C.) and subsequent lysis with 1 mg/ml lysozyme in phosphate buffer (Buffer A; 0.1M pH7.2) containing 0.5M NaCl) for one hour and subsequent sonication (3 cycles of 10 second pulses in sonicating water bath) the soluble and insoluble forms of the proteins of interest were separated by centrifugation at 13,000×g for 10 minutes. The precipitate was then resuspended in Buffer A containing 8M urea by freeze/thawing (3 cycles of freezing at -80° C. for 10 minutes and subsequent thawing to room temperature) and sonication (3 cycles of 10 second pulses in sonicating water bath), and subsequent centrifugation for 25 minutes at 18,000×g). The over expressed proteins of interest in the supernatant and the solubilised pellet were purified by initial specific binding (through their His-tag) to a nickel (NiSO<sub>4</sub>)-bound Sepharose chromatography column (Ni-Sepharose) and elution with an imidazole solution run through the column in the following stepwise manner: 5% for 5 minutes, 30% for 60 minutes, 35% for 60 minutes, 50% for 100 minutes and 55% for 100 minutes. Fractions from this stepwise elution were analysed in acrylamide denaturing gels with a 4% acrylamide/bis-acrylamide stacking layer and a 12% acrylamide/bis-acrylamide separating layer. The fractions containing the over expressed proteins of interest were pooled and dialyzed against sterile phosphate buffer (8 g NaCl, 0.2 g KCl, 1.44 g Na<sub>2</sub>HPO<sub>4</sub>, 0.24 g KH<sub>2</sub>PO<sub>4</sub>, per liter of distilled H<sub>2</sub>O, pH 7.4).

All the proteins of interest were successfully over expressed from the indicated strains and under the indicated conditions. They were also subsequently extracted from the total cellular protein content of the over expressing *E. coli* strains with more than 95% purity. Examples of the purification obtained for each of the proteins are indicated below.

Evaluation of Vaccination-Mediated Protection of Balb/C Mice Against Infection by *S. aureus*

One week after the second boost each animal was infected with an i.v. (tail vein) injection of 100 microliters of endotoxin-free PBS containing  $1.1 \times 10^7$  ( $\pm 0.5 \times 10^7$ ) cells of *S. aureus* strain Newman. The latter were prepared from cultures growing to early stationary phase in Brain Heart Infusion medium (BHI), which were then washed three times with the same volume of PBS.

After 10 to 14 days the animals were sacrificed according to Schedule 1 cervical dislocation. The pair of kidneys from each animal was extracted in aseptic conditions, and homogenized in sterile PBS. Serial dilutions of the kidney homoge-

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nates were carried out in PBS and plated on BHI agar plates. Plates containing between 10 to 150 staphylococcal colonies were counted and dilution corrected. The number of viable cells in the kidneys was inferred from the number of colony forming units (CFU) on the plates. Evaluation of the possible protection against infection conferred by vaccination with DivIB-2 was determined from difference in the number of *S. aureus* cells in the kidneys of animals vaccinated with KLH and those vaccinated with DivIB-2. The statistic significance of the difference was calculated using the Mann-Whitney test. A significantly higher ( $p<0.05$ ) number of *S. aureus* in KLH vaccinated animals compared to the DivIB-2 vaccinated animals was concluded as protection.

Vaccination: Generic Protocol for Polyvalent Vaccines

Combination (or polyvalent) vaccines including variations of the antigens (conjugated selected PheP peptide, YdiE, DivIB, DivIC and FtsL) will follow an identical protocol with the following modifications. The vaccine priming and boost mixtures will contain rather than a single component 2 or more of the components. The total volume of mixed vaccine used for priming and boosting injections will fluctuate in a range of 50-100 microliters per animal. Similarly the total amount in each of those injections may vary between 50-100 micrograms. The amount of each antigen to contribute to the total amount of vaccine in the priming or boosting mix will vary between 20% to 80% of the total.

The various combinations of antigens to be evaluated as a vaccine mix will be undertaken according to the matrix in Table 2. The combinations are grouped in 3 tiers. Depending on results from the 1<sup>st</sup> Tier of experiments the 2<sup>nd</sup> Tier of experiments would be undertaken accordingly, and depending on the results from the latter the 3<sup>rd</sup> Tier will be undertaken. In each Tier a vaccination experiment will contain an antigen in the Y axis, together with those ticked along the X axis, and labelled with the same colour. Each vaccination experiment is labelled with a different colour.

## EXAMPLE 1

The experimental sample consisted in a combination antigen of the extracellular domains of YdiE and DivIB. The amount of antigen administered to each mouse (Female Balb/C, approx. 5-6 weeks old) was 5 ug of YdiE plus 50 ug of

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DivIB. Those amounts were contained within 100 ul of eluent consisting on a 50:50 v:v of PBS (Phosphate Buffer Saline) and Complete Freund's Adjuvant (used for the vaccination priming) or Incomplete Freund's Adjuvant (used for the vaccination boost). Priming was undertaken day 0, Boost 1 at 14 days, and Boost 2 at 21 days. Subsequently, 7 days later, i.e., at day 28 the animals were infected with *Staphylococcus aureus* strain Newman. Each test group (control and experimental) had 10 animals. The bacterial dose administered to the animals (both, control and experimental) contained  $4 \times 10^6$  bacteria in 100 ul of PBS. The infection period was run for 3 days, and the weight of the animals was monitored daily (we also extracted organs to evaluate bacterial loads in organs, Table 4). At that point the animals were sacrificed. The output of the experiment was calculated as the percentage body weight loss between day 3 and day 0 for every animal. The results of these experiments are shown in Table 3. Statistical analysis of data in Table 3: TEST: Non-parametric statistical hypothesis test—Mann-Whitney U

SELECTED OPTIONS: Two-tailed, unpaired, 95% confidence interval.

RESULTS: (two group comparison)

II and I:  $p=0.622$

III and I:  $p=0.039^*$

IV and I:  $p=0.001^*$

II and III:  $p=0.061$

II and IV:  $p=0.008^*$

III and IV:  $p=0.158$

\*comparisons with statistically significant difference between the groups

Statistical analysis Table 4:

TEST: Non-parametric statistical hypothesis test—Mann-Whitney U

SELECTED OPTIONS: Two-tailed, unpaired, 95% confidence interval.

RESULTS: (two group comparison)

II and I:  $p=0.2$

III and I:  $p=0.105$

IV and I:  $p=0.009^*$

II and III:  $p=0.378$

II and IV:  $p=0.131$

III and IV:  $p=0.504$

\*comparisons with statistically significant difference between the groups

TABLE 1

Oligonucleotide sequences						
Progenitor gene name	Code - complete gene progenitor sequence	Code - fragment sequence amplified from progenitor	Oligonucleotide name	Oligonucleotide sequence code	Oligonucleotide sequence	Name of the resulting over-expression plasmids
ydiE/gcp	Sequence 2	Sequence 21	5'GLUSh318B	Sequence 29	ATAATACCATGGCTGTTTCATCATATTGCAGGAC	pGL597
divIB	Sequence 3	Sequence 22	3'GLUSh318B 5'GLUSh341C	Sequence 30 Sequence 31	ATAATACTCGAGTTCTGCAGAATACTCTTCTAAATC ATAATACCATGGCTCCACTTAGTAAATATGCGCATG	pGL601
divIC	Sequence 4	Sequence 23	3'GLUSh341C ALB21	Sequence 32 Sequence 33	ATAATACTCGAGATTATTCTTACTTGATTGTTTG ATAATACCATGGCTAAACATCGCAATGATATTGAT	pALB26
ftsL	Sequence 5	Sequence 24	ALB22 ALB19	Sequence 34 Sequence 35	ATAATTCTCGAGTTTTCGAAGATTTTGAGCT ATAATACCATGGCTAAATGGATGCGTATGATACG	pALB27
			ALB20	Sequence 36	ATAATACTCGAGATTTTTCGCTTCGCCATTACT	

CCATGG: NcoI  
CTCGAG: XhoI

TABLE 2

Multivalent vaccine experiments: Vaccine combinations												
	Antigen											
	Tier 1				Tier 2				Tier 3			
	YdiE	DivIB	DivIC	FtsL SEQ 5 SEQ 10 SEQ 19 SEQ 24	YdiE	DivIB	DivIC	FtsL	YdiE	DivIB	DivIC	FtsL
PheP	✓	✓	✓	✓								
SEQ 1	✓	✓										
SEQ 6							✓	✓				
SEQ 15									✓			
SEQ 20												
											✓	
												✓
YdiE		✓										
SEQ 2						✓	✓	✓				
SEQ 7							✓	✓				
SEQ 16											✓	
SEQ 21												✓
DivIB			✓	✓								
SEQ 3							✓					
SEQ 8								✓				
SEQ 17												
SEQ 22												
DivIC								✓				
SEQ 4												
SEQ 9												
SEQ 18												
SEQ 23												

TABLE 3

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TABLE 4

% Body Weight Loss					Log10 CFUs in Kidneys per animal						
Experimental Samples					45	Control Sample		Experimental Samples			
Control Sample I Animal Number	Adjuvant alone (Freunds)	II Antigen: rYdiE	III Antigen: rDivIB	IV Combination Antigen: rYdiE rDivIB		Animal Number	I Adjuvant alone (Freunds)	II Antigen: rYdiE	III Antigen: rDivIB	IV Combination Antigen: rYdiE rDivIB	
1	11.1	11.3	13.1	2.3	50	1	7.82	6.98	5.6	6.04	
2	12.7	4.3	0.0	2.0		2	7.73	6.5	6.5	6.12	
3	9.7	9.0	3.5	0.0		55	3	7.7	5.61	4.64	5.97
4	7.6	12.6	0.5	-4.3			4	6.98	7.61	5.99	5.61
5	9.4	1.0	7.1	-0.5			5	6.74	5.09	6.54	5.38
6	9.9	6.2	3.3	1.8	6		7.32	6.38	6.03	5.88	
7	2.0	3.8	2.1	1.5	60		7	6.5	6.6	6.41	6.74
8	4.2	5.3	1.9	1.4		8	6.2	6.75	6.66	5.96	
9	1.0	3.4	1.0	1.6		9	5.61	6.72	7.88	6.98	
10	3.1	7.0	6.8	3.9		10	6.06	6.63	6.63	6.68	
11	7.7	4.7	-2.5	-0.5		65	11	7.04	6.45		4.74



## SEQUENCE LISTING

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<211> LENGTH: 1455

<212> TYPE: DNA

<213> ORGANISM: *Staphylococcus aureus*

<400> SEQUENCE: 1

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aataaggtec taccatataa agcacctttt tatccattag gaccaatcat tgcatcact   1260
acactattat tcttgctatt tgggtggtca gttgaatata ttttaaaaga tcaatgggta   1320
aatgctttta aaaacttttt acctttaatc attctagcgt tgatttactt tattcataaa   1380
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<212> TYPE: DNA

<213> ORGANISM: *Staphylococcus aureus*

<400> SEQUENCE: 2

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aaacgatttg gcggtgtcgt tcccgaaagt gcaagtagac atcacgttga aggtataaca    180
gcaacaataa acgaggctct aggggatgcc gatgtatcaa tagaagatat tgatgccata    240
gcggttacag aaggccctgg actaattggt gcgttactaa taggtgttaa tgcagccaaa    300
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ccagtggtgc cacaagttga tcggttggct gctgaagggtg aagataactta ttcattccct	600
cgtgtttggt tggataaaga tagttatgat tttagtttta gtgggttgaa aagtgccgta	660
atcaatcaac ttcacaatca acgacaaaaa aatattccaa tcattgaagc taacgtagca	720
acgagctttc aaaacagtgt tgtagagggtg ctcacgttta aagctattca agcttgtaaa	780
gaatatggtg ttcagcgatt aattgttgct ggtggcgtgg cgagtaataa aggattacgt	840
caatctttag cggatcaatg caaagtcaat gacattcaat taactatccc aagtcctaaa	900
ttatgcacag ataatgctgc aatgataggc gttgccggcc actatttgta tcagcaaggt	960
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&lt;211&gt; LENGTH: 1320

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Staphylococcus aureus

&lt;400&gt; SEQUENCE: 3

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agtcatgcga atgataataa tatcgatgat tctacagact ctaatatga aaatgaggat	300
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ttgttgattg ctgttatatt aatttacatg ttttcaccac ttagtaaaat tgcgcattga	600
aatataaatg gaaataatca cgttagtact tcaaagataa acaaagtttt aggtgttaaa	660
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 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: selected pheP peptide DNA sequence

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 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: extramembranous ydiE/gcp sequence

<400> SEQUENCE: 7

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tcatttgaag tcattgttga aacacgagat gacgcagtag gtgaggctta tgataaagtg    180
gcacgaacaa ttggtttaaa ttatccaggt ggtccacaag ttgatcggtt ggctgctgaa    240
ggatgaagata cttattcatt cctctgtgtt tggttggata aagatagtta tgattttagt    300
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ccaatcattg aagctaactg agcaacgagc tttcaaaaaca gtgtttaga ggtgctcacg    420
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gtggcgagta ataaaggatt acgtcaatct ttagcggatc aatgcaaagt caatgacatt 540
caattaacta tcccaagtcc taaattatgc acagataatg ctgcaatgat aggcgttgcc 600
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<210> SEQ ID NO 8
<211> LENGTH: 741
<212> TYPE: DNA
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<223> OTHER INFORMATION: extramembranous divIB sequence, also named in
preceding patent DivIB-1

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<400> SEQUENCE: 8

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gctattaatg atctcgaaga ggatccatta atcaaaagtg ttgagataga caagcaatta 180
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<210> SEQ ID NO 9
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: extramembranous divIC sequence

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<400> SEQUENCE: 9

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attgaaaaaa ttgcgcgtga tgattattac ttaagcaaca aaggtgaagt gatttttagg 180
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<210> SEQ ID NO 10
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<212> TYPE: DNA
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atatacgaaa aggtaagaa acaggggatg agccttgaga acgataatgt aaaggtagt 180

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 cgtagtaatg gcgaagcaaa aaat 204

<210> SEQ ID NO 11  
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 <220> FEATURE:  
 <223> OTHER INFORMATION: (T7-tag / intermediate bases / ydiE  
 extramembranous / intermediate bases / His-tag sequence

&lt;400&gt; SEQUENCE: 11

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catttatcat ttgaagtcac tggtgaaaca cgagatgacg cagtaggtga ggcttatgat	180
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gggtggcgtgg cgagtaataa aggattacgt caatctttag cggatcaatg caaagtcaat	540
gacattcaat taactatccc aagtcctaaa ttatgcacag ataagtctgc aatgataggc	600
gttgccggcc actatttgta tcagcaaggt cgatttgctg atttagcatt aaatgggcac	660
agcaatatag atttagaaga gtattctgca gaactcgagc accaccacca ccaccactga	720

<210> SEQ ID NO 12  
 <211> LENGTH: 774  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: T7-tag / intermediate bases / divIB  
 extramembranous / intermediate bases / His-tag sequence

&lt;400&gt; SEQUENCE: 12

atggctccac ttagtaaaat tgcgcagtga aatataaatg gaaataatca cgtagtagtact	60
tcaaagataa acaaagtttt aggtgttaaa aatgattcga ggatgtatgc gtttagtaaa	120
aaaaatgcta ttaatgatct cgaagaggat ccattaatca aaagtgttga gatacacaag	180
caattaccaa acacattaaa cgtagatata acagaaaatg aaattattgc ttagtgaaa	240
tataaaggta aatatttacc tttattagaa aatggtaaat tgcttaaagg ttcaaatgat	300
gtcaaaaatta atgatgcacc tgctcatggat gggttcaaaag gtacaaaaga agatgatatg	360
attaaggcgt tatctgaaat gacacctgaa gttagacgat atattgccga agtgacatac	420
gccccaaagta aaaacaaaca aagcagaatt gaattgttta cgacagatgg acttcaagta	480
atcggtgata tttcgacgat atctaagaaa atgaaatatt atccgcagat gtcacaatca	540
ttatcaaggg atagttcggg taaactaaaa acaagaggct atattgattt atcagtcggg	600
gcttcattta tccataaccg tggaaacacg tctagtcaat cagaaagcga taaaaatgtg	660
actaaatcat ctcaagagga aaatcaagca aaagaagaat tacaaagcgt tttaaacaaa	720
attaacaaac aatcaagtaa gaataatctc gagcaccacc accaccacca ctga	774

<210> SEQ ID NO 13  
 <211> LENGTH: 255  
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T7-tag / intermediate bases /
      divIC extramembranous / intermediate bases / His-tag sequence

<400> SEQUENCE: 13

atggcctaaac atcgcaatga tattgatgca caggagcgaa aagcgaaaga agcacagttt      60
caaaagcaac aaaatgaaga aattgcggtta aaagaaaagt tgaataatct gaatgacaaa      120
gattacattg aaaaaattgc gcgtgatgat tattacttaa gcaacaaagg tgaagtgatt      180
tttaggttgc cagaagacaa agattcgtct agctcaaaat cttcgaaaaa actcgagcac      240
caccaccacc accac                                          255

<210> SEQ ID NO 14
<211> LENGTH: 234
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T7-tag / intermediate bases / ftsL
      extramembranous / intermediate bases / His-tag sequence

<400> SEQUENCE: 14

atggctaaaa tggatgcgta tgatacgga ggaaagattg cagatttaga ttataaaata      60
gataaacaat caagtgaaaa cagtgcctta caatctgaaa tcaaaaagaa ttcttcttat      120
gaacgcatat acgaaaaggc taagaacag gggatgagcc ttgagaacga taatgtaaag      180
gtagtgcgta gtaatggcga agcaaaaaat ctcgagcacc accaccacca ccac      234

<210> SEQ ID NO 15
<211> LENGTH: 484
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 15

Met Glu Asp Asn Lys Met Asn Arg Ser Leu Asn Ser Arg His Ile Ser
1      5      10      15
Met Ile Ala Ile Gly Gly Ala Ile Gly Thr Gly Leu Phe Val Ala Thr
20     25     30
Gly Asn Ile Ile Ser Gln Ala Gly Pro Gly Gly Ala Ile Leu Ala Tyr
35     40     45
Leu Val Ile Gly Val Met Leu Tyr Phe Leu Met Ser Ser Ile Gly Glu
50     55     60
Leu Ala Thr Phe Tyr Pro Val Ser Gly Ser Phe Ser Ser Tyr Ser Thr
65     70     75     80
Arg Phe Ile Asp Ser Ser Leu Gly Phe Thr Met Gly Trp Leu Tyr Trp
85     90     95
Ala Leu Trp Ser Leu Val Thr Ser Val Asp Val Ile Val Ala Ser Asn
100    105    110
Val Leu Tyr Phe Trp Asp Thr Phe Lys Phe Phe His Pro Ile Thr Trp
115    120    125
Ser Leu Ile Phe Ile Thr Ile Leu Leu Leu Leu Asn Ile Phe Ser Val
130    135    140
Lys Ser Phe Gly Glu Thr Glu Phe Trp Leu Ser Leu Ile Lys Val Leu
145    150    155    160
Thr Ile Ile Val Phe Val Ile Phe Gly Phe Leu Met Ile Phe Gly Ile
165    170    175
Leu Gly Gly His Thr Tyr Gly Phe Glu Asn Tyr Thr Lys Gly Gln Ala
180    185    190

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Pro Phe Val Gly Gly Ile Ser Gly Phe Leu Gly Val Leu Leu Val Ala  
 195 200 205  
 Gly Phe Ser Val Gly Gly Thr Glu Val Val Ala Val Thr Ala Gly Glu  
 210 215 220  
 Ser Asp Asp Pro Lys Lys Ser Met Pro Lys Ala Ile Lys Gln Val Phe  
 225 230 235 240  
 Trp Arg Ile Leu Leu Phe Tyr Val Leu Ser Ile Ala Val Ile Gly Ala  
 245 250 255  
 Ile Ile Pro Tyr Thr Asp Pro Ser Leu Leu Arg Ala Ser Ser Ser Ile  
 260 265 270  
 Ser Gln Ser Pro Phe Thr Ile Val Phe Asp Arg Val Gly Ile Ala Phe  
 275 280 285  
 Ala Ala Ser Val Ile Asn Ala Val Ile Leu Thr Ser Leu Leu Ser Ala  
 290 295 300  
 Ala Asn Ser Gly Val Tyr Thr Thr Gly Arg Met Leu Tyr Ser Leu Ser  
 305 310 315 320  
 Ser Asp Lys Lys Ala Pro Gln Phe Leu Ser Lys Leu Asn Lys Thr Thr  
 325 330 335  
 Lys Leu Pro Leu Arg Ala Leu Leu Thr Thr Tyr Ala Val Val Val Ile  
 340 345 350  
 Val Ile Ile Tyr Ala Asn Phe Asn Ser Asn Ala Val Phe Asn Leu Leu  
 355 360 365  
 Glu Ile Ile Gly Ser Met Ile Ile Val Val Trp Gly Ser Ser Ile Trp  
 370 375 380  
 Ser Gln Ile Arg Leu Arg Gln Ala Ile Lys Lys Gln Gly Gln Asp Pro  
 385 390 395 400  
 Asn Lys Val Leu Pro Tyr Lys Ala Pro Phe Tyr Pro Leu Gly Pro Ile  
 405 410 415  
 Ile Val Ile Thr Thr Leu Leu Phe Leu Leu Phe Gly Gly Ser Val Glu  
 420 425 430  
 Tyr Ile Leu Lys Asp Gln Trp Leu Asn Ala Phe Lys Asn Phe Leu Pro  
 435 440 445  
 Leu Ile Ile Leu Ala Leu Ile Tyr Phe Ile His Lys Ile Ile His Lys  
 450 455 460  
 Thr Lys Phe Val Lys Leu Glu Thr Ile Asn Leu Lys Pro His Asp Tyr  
 465 470 475 480  
 Asp Asn Gln Lys

<210> SEQ ID NO 16  
 <211> LENGTH: 341  
 <212> TYPE: PRT  
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 16

Met Thr Lys Asp Ile Leu Ile Leu Ala Val Glu Thr Ser Cys Asp Glu  
 1 5 10 15  
 Thr Ser Val Ser Val Ile Lys Asn Gly Arg Asp Ile Leu Ser Asn Thr  
 20 25 30  
 Val Leu Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro  
 35 40 45  
 Glu Val Ala Ser Arg His His Val Glu Gly Ile Thr Ala Thr Ile Asn  
 50 55 60  
 Glu Ala Leu Gly Asp Ala Asp Val Ser Ile Glu Asp Ile Asp Ala Ile  
 65 70 75 80

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Ala Val Thr Glu Gly Pro Gly Leu Ile Gly Ala Leu Leu Ile Gly Val  
85 90 95

Asn Ala Ala Lys Ala Leu Ala Phe Ala Tyr Asp Lys Pro Leu Ile Pro  
100 105 110

Val His His Ile Ala Gly His Ile Tyr Ala Asn His Ile Glu Glu Pro  
115 120 125

Leu Thr Phe Pro Leu Ile Ala Leu Ile Val Ser Gly Gly His Thr Glu  
130 135 140

Leu Val Tyr Met Lys Asp His Leu Ser Phe Glu Val Ile Gly Glu Thr  
145 150 155 160

Arg Asp Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Ala Arg Thr Ile  
165 170 175

Gly Leu Asn Tyr Pro Gly Gly Pro Gln Val Asp Arg Leu Ala Ala Glu  
180 185 190

Gly Glu Asp Thr Tyr Ser Phe Pro Arg Val Trp Leu Asp Lys Asp Ser  
195 200 205

Tyr Asp Phe Ser Phe Ser Gly Leu Lys Ser Ala Val Ile Asn Gln Leu  
210 215 220

His Asn Gln Arg Gln Lys Asn Ile Pro Ile Ile Glu Ala Asn Val Ala  
225 230 235 240

Thr Ser Phe Gln Asn Ser Val Val Glu Val Leu Thr Phe Lys Ala Ile  
245 250 255

Gln Ala Cys Lys Glu Tyr Gly Val Gln Arg Leu Ile Val Ala Gly Gly  
260 265 270

Val Ala Ser Asn Lys Gly Leu Arg Gln Ser Leu Ala Asp Gln Cys Lys  
275 280 285

Val Asn Asp Ile Gln Leu Thr Ile Pro Ser Pro Lys Leu Cys Thr Asp  
290 295 300

Asn Ala Ala Met Ile Gly Val Ala Gly His Tyr Leu Tyr Gln Gln Gly  
305 310 315 320

Arg Phe Ala Asp Leu Ala Leu Asn Gly His Ser Asn Ile Asp Leu Glu  
325 330 335

Glu Tyr Ser Ala Glu  
340

&lt;210&gt; SEQ ID NO 17

&lt;211&gt; LENGTH: 439

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus aureus

&lt;400&gt; SEQUENCE: 17

Met Asp Asp Lys Thr Lys Asn Asp Gln Gln Glu Ser Asn Glu Asp Lys  
1 5 10 15

Asp Glu Leu Glu Leu Phe Thr Arg Asn Thr Ser Lys Lys Arg Arg Gln  
20 25 30

Arg Lys Arg Ser Lys Ala Thr His Phe Ser Asn Gln Asn Lys Asp Asp  
35 40 45

Thr Ser Gln Gln Ala Asp Phe Asp Glu Glu Ile Tyr Leu Ile Asn Lys  
50 55 60

Asp Phe Lys Lys Glu Glu Ser Asn Asp Lys Asn Asn Asp Ser Ala Ser  
65 70 75 80

Ser His Ala Asn Asp Asn Asn Ile Asp Asp Ser Thr Asp Ser Asn Ile  
85 90 95

Glu Asn Glu Asp Tyr Arg Tyr Asn Gln Glu Ile Asp Asp Gln Asn Glu



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100					105					110					
Ser	Asn	Val	Ile	Ser	Val	Asp	Asn	Glu	Gln	Pro	Gln	Ser	Ala	Pro	Lys
	115						120					125			
Glu	Gln	Asn	Ser	Asp	Ser	Ile	Asp	Glu	Glu	Thr	Val	Thr	Lys	Lys	Glu
	130					135					140				
Arg	Lys	Ser	Lys	Val	Thr	Gln	Leu	Lys	Pro	Leu	Thr	Leu	Glu	Glu	Lys
	145					150					155				160
Arg	Lys	Leu	Arg	Arg	Lys	Arg	Gln	Lys	Arg	Ile	Gln	Tyr	Ser	Val	Ile
			165						170					175	
Thr	Ile	Leu	Val	Leu	Leu	Ile	Ala	Val	Ile	Leu	Ile	Tyr	Met	Phe	Ser
		180						185					190		
Pro	Leu	Ser	Lys	Ile	Ala	His	Val	Asn	Ile	Asn	Gly	Asn	Asn	His	Val
	195						200					205			
Ser	Thr	Ser	Lys	Ile	Asn	Lys	Val	Leu	Gly	Val	Lys	Asn	Asp	Ser	Arg
	210					215					220				
Met	Tyr	Thr	Phe	Ser	Lys	Lys	Asn	Ala	Ile	Asn	Asp	Leu	Glu	Glu	Asn
	225					230					235				240
Pro	Leu	Ile	Lys	Ser	Val	Glu	Ile	His	Lys	Gln	Leu	Pro	Asn	Thr	Leu
			245						250					255	
Asn	Val	Asp	Ile	Thr	Glu	Asn	Glu	Ile	Ile	Ala	Leu	Val	Lys	Tyr	Lys
		260					265						270		
Gly	Lys	Tyr	Leu	Pro	Leu	Leu	Glu	Asn	Gly	Lys	Leu	Leu	Lys	Gly	Ser
	275						280					285			
Asn	Asp	Val	Lys	Ile	Asn	Asp	Ala	Pro	Val	Met	Asp	Gly	Phe	Lys	Gly
	290					295					300				
Thr	Lys	Glu	Asp	Asp	Met	Ile	Lys	Ala	Leu	Ser	Glu	Met	Thr	Pro	Glu
	305					310					315				320
Val	Arg	Arg	Tyr	Ile	Ala	Glu	Val	Thr	Tyr	Ala	Pro	Ser	Lys	Asn	Lys
			325						330					335	
Gln	Ser	Arg	Ile	Glu	Leu	Phe	Thr	Thr	Asp	Gly	Leu	Gln	Val	Ile	Gly
		340					345						350		
Asp	Ile	Ser	Thr	Ile	Ser	Lys	Lys	Met	Lys	Tyr	Tyr	Pro	Gln	Met	Ser
	355						360					365			
Gln	Ser	Leu	Ser	Arg	Asp	Ser	Ser	Gly	Lys	Leu	Lys	Thr	Arg	Gly	Tyr
	370					375					380				
Ile	Asp	Leu	Ser	Val	Gly	Ala	Ser	Phe	Ile	Pro	Tyr	Arg	Gly	Asn	Thr
	385					390					395				400
Ser	Ser	Gln	Ser	Glu	Ser	Asp	Lys	Asn	Val	Thr	Lys	Ser	Ser	Gln	Glu
			405						410					415	
Glu	Asn	Gln	Ala	Lys	Glu	Glu	Leu	Gln	Ser	Val	Leu	Asn	Lys	Ile	Asn
		420					425						430		
Lys	Gln	Ser	Ser	Lys	Asn	Asn									
	435														

&lt;210&gt; SEQ ID NO 18

&lt;211&gt; LENGTH: 130

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus aureus

&lt;400&gt; SEQUENCE: 18

Met	Lys	Asn	Lys	Val	Glu	His	Ile	Glu	Asn	Gln	Tyr	Thr	Ser	Gln	Glu
1			5						10					15	

Asn	Lys	Lys	Lys	Gln	Arg	Gln	Lys	Met	Lys	Met	Arg	Val	Val	Arg	Arg
	20						25					30			

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Arg Ile Thr Val Phe Ala Gly Val Leu Leu Ala Ile Ile Val Val Leu  
           35                  40                  45

Ser Ile Leu Leu Val Val Gln Lys His Arg Asn Asp Ile Asp Ala Gln  
       50                  55                  60

Glu Arg Lys Ala Lys Glu Ala Gln Phe Gln Lys Gln Gln Asn Glu Glu  
       65                  70                  75                  80

Ile Ala Leu Lys Glu Lys Leu Asn Asn Leu Asn Asp Lys Asp Tyr Ile  
           85                  90                  95

Glu Lys Ile Ala Arg Asp Asp Tyr Tyr Leu Ser Asn Lys Gly Glu Val  
           100                  105                  110

Ile Phe Arg Leu Pro Glu Asp Lys Asp Ser Ser Ser Ser Lys Ser Ser  
       115                  120                  125

Lys Lys  
       130

<210> SEQ ID NO 19  
 <211> LENGTH: 133  
 <212> TYPE: PRT  
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 19

Met Ala Val Glu Lys Val Tyr Gln Pro Tyr Asp Glu Gln Val Tyr Asn  
 1          5                  10                  15

Ser Ile Pro Lys Gln Gln Pro Gln Thr Lys Pro Glu Lys Lys Thr Val  
       20                  25                  30

Ser Arg Lys Val Val Val Gln Leu Thr Lys Phe Glu Lys Val Leu Tyr  
       35                  40                  45

Ile Thr Leu Ile Thr Val Ile Ala Met Leu Ser Ile Tyr Met Leu Ser  
       50                  55                  60

Leu Lys Met Asp Ala Tyr Asp Thr Arg Gly Lys Ile Ala Asp Leu Asp  
       65                  70                  75                  80

Tyr Lys Ile Asp Lys Gln Ser Ser Glu Asn Ser Ala Leu Gln Ser Glu  
       85                  90                  95

Ile Lys Lys Asn Ser Ser Tyr Glu Arg Ile Tyr Glu Lys Ala Lys Lys  
       100                  105                  110

Gln Gly Met Ser Leu Glu Asn Asp Asn Val Lys Val Val Arg Ser Asn  
       115                  120                  125

Gly Glu Ala Lys Asn  
       130

<210> SEQ ID NO 20  
 <211> LENGTH: 14  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: selected extramembranous PheP sequence

<400> SEQUENCE: 20

Leu Tyr Phe Trp Asp Thr Phe Lys Phe Phe His Pro Ile Thr  
 1          5                  10

<210> SEQ ID NO 21  
 <211> LENGTH: 229  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: extramembranous YdiE sequence

<400> SEQUENCE: 21

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Val His His Ile Ala Gly His Ile Tyr Ala Asn His Ile Glu Glu Pro  
 1 5 10 15  
 Leu Thr Phe Pro Leu Ile Ala Leu Ile Val Ser Gly Gly His Thr Glu  
 20 25 30  
 Leu Val Tyr Met Lys Asp His Leu Ser Phe Glu Val Ile Gly Glu Thr  
 35 40 45  
 Arg Asp Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Ala Arg Thr Ile  
 50 55 60  
 Gly Leu Asn Tyr Pro Gly Gly Pro Gln Val Asp Arg Leu Ala Ala Glu  
 65 70 75 80  
 Gly Glu Asp Thr Tyr Ser Phe Pro Arg Val Trp Leu Asp Lys Asp Ser  
 85 90 95  
 Tyr Asp Phe Ser Phe Ser Gly Leu Lys Ser Ala Val Ile Asn Gln Leu  
 100 105 110  
 His Asn Gln Arg Gln Lys Asn Ile Pro Ile Ile Glu Ala Asn Val Ala  
 115 120 125  
 Thr Ser Phe Gln Asn Ser Val Val Glu Val Leu Thr Phe Lys Ala Ile  
 130 135 140  
 Gln Ala Cys Lys Glu Tyr Gly Val Gln Arg Leu Ile Val Ala Gly Gly  
 145 150 155 160  
 Val Ala Ser Asn Lys Gly Leu Arg Gln Ser Leu Ala Asp Gln Cys Lys  
 165 170 175  
 Val Asn Asp Ile Gln Leu Thr Ile Pro Ser Pro Lys Leu Cys Thr Asp  
 180 185 190  
 Asn Ala Ala Met Ile Gly Val Ala Gly His Tyr Leu Tyr Gln Gln Gly  
 195 200 205  
 Arg Phe Ala Asp Leu Ala Leu Asn Gly His Ser Asn Ile Asp Leu Glu  
 210 215 220  
 Glu Tyr Ser Ala Glu  
 225

&lt;210&gt; SEQ ID NO 22

&lt;211&gt; LENGTH: 247

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: extramembraneous DivIB sequence, also named in preceding patent DivIB-1

&lt;400&gt; SEQUENCE: 22

Pro Leu Ser Lys Ile Ala His Val Asn Ile Asn Gly Asn Asn His Val  
 1 5 10 15  
 Ser Thr Ser Lys Ile Asn Lys Val Leu Gly Val Lys Asn Asp Ser Arg  
 20 25 30  
 Met Tyr Thr Phe Ser Lys Lys Asn Ala Ile Asn Asp Leu Glu Glu Asp  
 35 40 45  
 Pro Leu Ile Lys Ser Val Glu Ile His Lys Gln Leu Pro Asn Thr Leu  
 50 55 60  
 Asn Val Asp Ile Thr Glu Asn Glu Ile Ile Ala Leu Val Lys Tyr Lys  
 65 70 75 80  
 Gly Lys Tyr Leu Pro Leu Leu Glu Asn Gly Lys Leu Leu Lys Gly Ser  
 85 90 95  
 Asn Asp Val Lys Ile Asn Asp Ala Pro Val Met Asp Gly Phe Lys Gly  
 100 105 110  
 Thr Lys Glu Asp Asp Met Ile Lys Ala Leu Ser Glu Met Thr Pro Glu  
 115 120 125

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Val Arg Arg Tyr Ile Ala Glu Val Thr Tyr Ala Pro Ser Lys Asn Lys  
 130 135 140

Gln Ser Arg Ile Glu Leu Phe Thr Thr Asp Gly Leu Gln Val Ile Gly  
 145 150 155 160

Asp Ile Ser Thr Ile Ser Lys Lys Met Lys Tyr Tyr Pro Gln Met Ser  
 165 170 175

Gln Ser Leu Ser Arg Asp Ser Ser Gly Lys Leu Lys Thr Arg Gly Tyr  
 180 185 190

Ile Asp Leu Ser Val Gly Ala Ser Phe Ile Pro Tyr Arg Gly Asn Thr  
 195 200 205

Ser Ser Gln Ser Glu Ser Asp Lys Asn Val Thr Lys Ser Ser Gln Glu  
 210 215 220

Glu Asn Gln Ala Lys Glu Glu Leu Gln Ser Val Leu Asn Lys Ile Asn  
 225 230 235 240

Lys Gln Ser Ser Lys Asn Asn  
 245

<210> SEQ ID NO 23  
 <211> LENGTH: 75  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: extramembraneous DivIC sequence

<400> SEQUENCE: 23

Lys His Arg Asn Asp Ile Asp Ala Gln Glu Arg Lys Ala Lys Glu Ala  
 1 5 10 15

Gln Phe Gln Lys Gln Gln Asn Glu Glu Ile Ala Leu Lys Glu Lys Leu  
 20 25 30

Asn Asn Leu Asn Asp Lys Asp Tyr Ile Glu Lys Ile Ala Arg Asp Asp  
 35 40 45

Tyr Tyr Leu Ser Asn Lys Gly Glu Val Ile Phe Arg Leu Pro Glu Asp  
 50 55 60

Lys Asp Ser Ser Ser Ser Lys Ser Ser Lys Lys  
 65 70 75

<210> SEQ ID NO 24  
 <211> LENGTH: 68  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: extramembraneous FtsL sequence

<400> SEQUENCE: 24

Lys Met Asp Ala Tyr Asp Thr Arg Gly Lys Ile Ala Asp Leu Asp Tyr  
 1 5 10 15

Lys Ile Asp Lys Gln Ser Ser Glu Asn Ser Ala Leu Gln Ser Glu Ile  
 20 25 30

Lys Lys Asn Ser Ser Tyr Glu Arg Ile Tyr Glu Lys Ala Lys Lys Gln  
 35 40 45

Gly Met Ser Leu Glu Asn Asp Asn Val Lys Val Val Arg Ser Asn Gly  
 50 55 60

Glu Ala Lys Asn  
 65

<210> SEQ ID NO 25  
 <211> LENGTH: 239  
 <212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T7-tag / intermediate bases / YdiE
      extramembranous / intermediate bases / His-tag sequence

<400> SEQUENCE: 25

Met Ala Val His His Ile Ala Gly His Ile Tyr Ala Asn His Ile Glu
1          5          10         15

Glu Pro Leu Thr Phe Pro Leu Ile Ala Leu Ile Val Ser Gly Gly His
          20          25          30

Thr Glu Leu Val Tyr Met Lys Asp His Leu Ser Phe Glu Val Ile Gly
          35          40          45

Glu Thr Arg Asp Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Ala Arg
          50          55          60

Thr Ile Gly Leu Asn Tyr Pro Gly Gly Pro Gln Val Asp Arg Leu Ala
          65          70          75          80

Ala Glu Gly Glu Asp Thr Tyr Ser Phe Pro Arg Val Trp Leu Asp Lys
          85          90          95

Asp Ser Tyr Asp Phe Ser Phe Ser Gly Leu Lys Ser Ala Val Ile Asn
          100         105         110

Gln Leu His Asn Gln Arg Gln Lys Asn Ile Pro Ile Ile Glu Ala Asn
          115         120         125

Val Ala Thr Ser Phe Gln Asn Ser Val Val Glu Val Leu Thr Phe Lys
          130         135         140

Ala Ile Gln Ala Cys Lys Glu Tyr Gly Val Gln Arg Leu Ile Val Ala
          145         150         155         160

Gly Gly Val Ala Ser Asn Lys Gly Leu Arg Gln Ser Leu Ala Asp Gln
          165         170         175

Cys Lys Val Asn Asp Ile Gln Leu Thr Ile Pro Ser Pro Lys Leu Cys
          180         185         190

Thr Asp Asn Ala Ala Met Ile Gly Val Ala Gly His Tyr Leu Tyr Gln
          195         200         205

Gln Gly Arg Phe Ala Asp Leu Ala Leu Asn Gly His Ser Asn Ile Asp
          210         215         220

Leu Glu Glu Tyr Ser Ala Glu Leu Glu His His His His His His
          225         230         235

<210> SEQ ID NO 26
<211> LENGTH: 257
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T7-tag / intermediate bases / DivIB
      extramembranous / intermediate bases / His-tag sequence; also
      termed DivB-2 in a preceding patent

<400> SEQUENCE: 26

Met Ala Pro Leu Ser Lys Ile Ala His Val Asn Ile Asn Gly Asn Asn
1          5          10         15

His Val Ser Thr Ser Lys Ile Asn Lys Val Leu Gly Val Lys Asn Asp
          20          25          30

Ser Arg Met Tyr Thr Phe Ser Lys Lys Asn Ala Ile Asn Asp Leu Glu
          35          40          45

Glu Asp Pro Leu Ile Lys Ser Val Glu Ile His Lys Gln Leu Pro Asn
          50          55          60

Thr Leu Asn Val Asp Ile Thr Glu Asn Glu Ile Ile Ala Leu Val Lys
          65          70          75          80

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Tyr	Lys	Gly	Lys	Tyr	Leu	Pro	Leu	Leu	Glu	Asn	Gly	Lys	Leu	Leu	Lys
				85					90					95	
Gly	Ser	Asn	Asp	Val	Lys	Ile	Asn	Asp	Ala	Pro	Val	Met	Asp	Gly	Phe
			100					105					110		
Lys	Gly	Thr	Lys	Glu	Asp	Asp	Met	Ile	Lys	Ala	Leu	Ser	Glu	Met	Thr
			115				120					125			
Pro	Glu	Val	Arg	Arg	Tyr	Ile	Ala	Glu	Val	Thr	Tyr	Ala	Pro	Ser	Lys
						135					140				
Asn	Lys	Gln	Ser	Arg	Ile	Glu	Leu	Phe	Thr	Thr	Asp	Gly	Leu	Gln	Val
145					150					155					160
Ile	Gly	Asp	Ile	Ser	Thr	Ile	Ser	Lys	Lys	Met	Lys	Tyr	Tyr	Pro	Gln
				165					170					175	
Met	Ser	Gln	Ser	Leu	Ser	Arg	Asp	Ser	Ser	Gly	Lys	Leu	Lys	Thr	Arg
			180					185					190		
Gly	Tyr	Ile	Asp	Leu	Ser	Val	Gly	Ala	Ser	Phe	Ile	Pro	Tyr	Arg	Gly
			195				200					205			
Asn	Thr	Ser	Ser	Gln	Ser	Glu	Ser	Asp	Lys	Asn	Val	Thr	Lys	Ser	Ser
						215					220				
Gln	Glu	Glu	Asn	Gln	Ala	Lys	Glu	Glu	Leu	Gln	Ser	Val	Leu	Asn	Lys
225					230					235					240
Ile	Asn	Lys	Gln	Ser	Ser	Lys	Asn	Asn	Leu	Glu	His	His	His	His	His
				245					250					255	

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<210> SEQ ID NO 27
<211> LENGTH: 85
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: (T7-tag / intermediate bases / DivIC
      extramembranous / intermediate bases / His-tag sequence

<400> SEQUENCE: 27

Met Ala Lys His Arg Asn Asp Ile Asp Ala Gln Glu Arg Lys Ala Lys
 1             5             10             15
Glu Ala Gln Phe Gln Lys Gln Gln Asn Glu Glu Ile Ala Leu Lys Glu
      20             25             30
Lys Leu Asn Asn Leu Asn Asp Lys Asp Tyr Ile Glu Lys Ile Ala Arg
      35             40             45
Asp Asp Tyr Tyr Leu Ser Asn Lys Gly Glu Val Ile Phe Arg Leu Pro
      50             55             60
Glu Asp Lys Asp Ser Ser Ser Lys Ser Ser Lys Lys Leu Glu His
65             70             75             80
His His His His His
      85

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<210> SEQ ID NO 28
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T7-tag / intermediate bases / ftsL
      extramembranous / intermediate bases / His-tag sequence

<400> SEQUENCE: 28

Met Ala Lys Met Asp Ala Tyr Asp Thr Arg Gly Lys Ile Ala Asp Leu
1             5             10            15

Asp Tyr Lys Ile Asp Lys Gln Ser Ser Glu Asn Ser Ala Leu Gln Ser

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20	25	30	
Glu Ile Lys Lys Asn Ser Ser Tyr Glu Arg Ile Tyr Glu Lys Ala Lys			
35	40	45	
Lys Gln Gly Met Ser Leu Glu Asn Asp Asn Val Lys Val Val Arg Ser			
50	55	60	
Asn Gly Glu Ala Lys Asn Leu Glu His His His His His His			
65	70	75	

<210> SEQ ID NO 29  
 <211> LENGTH: 33  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: nucleotide primer

<400> SEQUENCE: 29  
 ataataccat ggctgttcat catattgcag gac 33

<210> SEQ ID NO 30  
 <211> LENGTH: 36  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
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<400> SEQUENCE: 30  
 ataatactcg agttctgcag aatactcttc taaatc 36

<210> SEQ ID NO 31  
 <211> LENGTH: 36  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: nucleotide primer

<400> SEQUENCE: 31  
 ataataccat ggctccactt agtaaaattg cgcattg 36

<210> SEQ ID NO 32  
 <211> LENGTH: 34  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: nucleotide primer

<400> SEQUENCE: 32  
 ataatactcg agattattct tacttgattg ttg 34

<210> SEQ ID NO 33  
 <211> LENGTH: 35  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: nucleotide primer

<400> SEQUENCE: 33  
 ataataccat ggctaaacat cgcaatgata ttgat 35

<210> SEQ ID NO 34  
 <211> LENGTH: 33  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: nucleotide primer

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<400> SEQUENCE: 34

ataattctcg agtttttttcg aagattttga gct

33

<210> SEQ ID NO 35

<211> LENGTH: 35

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: nucleotide primer

<400> SEQUENCE: 35

ataataccat ggctaaaaatg gatgcgtatg atacg

35

<210> SEQ ID NO 36

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: nucleotide primer

<400> SEQUENCE: 36

ataatactcg agatttttttg cttcgccatt act

33

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The invention claimed is:

1. An immunogenic composition comprising two or more different isolated polypeptides wherein said immunogenic composition comprises:

- i) a polypeptide consisting of the amino acid sequence as represented in SEQ ID NO: 21; and
- ii) a polypeptide consisting of the amino acid sequence as represented in SEQ ID NO: 22.

2. The immunogenic composition according to claim 1, further comprising: a polypeptide comprising SEQ ID NO: 23.

3. The immunogenic composition according to claim 1, further comprising: a polypeptide comprising SEQ ID NO: 24.

4. The immunogenic composition according to claim 1, further comprising:

- i) a polypeptide comprising SEQ ID NO: 23; and
- ii) a polypeptide comprising SEQ ID NO: 24.

5. The immunogenic composition according to claim 1 further comprising at least one carrier and/or adjuvant.

6. The immunogenic composition according to claim 1, wherein said composition is adapted for administration as a nasal spray.

7. The immunogenic composition according to claim 1 wherein the composition is provided in an inhaler and delivered as an aerosol.

8. The immunogenic composition according to claim 1 wherein the composition includes at least one additional anti-bacterial agent.

9. A method for treating a *Staphylococcus aureus* infection in an animal subject, comprising administering an effective amount of an immunogenic composition according to claim 1.

10. The immunogenic composition of claim 5, wherein the adjuvant is selected from the group consisting of: aluminum hydroxide; aluminum phosphate; and calcium phosphate.

11. The immunogenic composition of claim 5, wherein said adjuvant is aluminum phosphate.

12. The composition of claim 11, wherein the adjuvant is formulated as a gel-type.

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